

RAW SEQUENCE LISTING

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Application Serial Number: 10/509, 464
Source: PCT
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DATE: 06/15/2005

PATENT APPLICATION: US/10/509,464

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3 <110> APPLICANT: NIEHRS, CHRISTOF
 4 MAO, BINGYU
 6 <120> TITLE OF INVENTION: COMPOSITIONS FOR DIAGNOSIS AND THERAPY OF DISEASES
 7 ASSOCIATED WITH ABERRANT EXPRESSION OF KREMEN AND/OR
 8 WNT
 10 <130> FILE REFERENCE: 31304-702.831
 12 <140> CURRENT APPLICATION NUMBER: 10/509,464
 C--> 13 <141> CURRENT FILING DATE: 2004-09-27
 15 <150> PRIOR APPLICATION NUMBER: PCT/EP03/03277
 16 <151> PRIOR FILING DATE: 2003-03-28
 18 <150> PRIOR APPLICATION NUMBER: EP 02 008 650.0
 19 <151> PRIOR FILING DATE: 2002-04-17
 21 <160> NUMBER OF SEQ ID NOS: 12
 23 <170> SOFTWARE: PatentIn Ver. 3.3
 25 <210> SEQ ID NO: 1
 26 <211> LENGTH: 1422
 27 <212> TYPE: DNA
 28 <213> ORGANISM: Mus musculus
 30 <400> SEQUENCE: 1
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 33 aggggaacac agagctggac agcgtgcaa ggtgggaagc catgtctgtt ctggaacgag 180
 34 actttccagc atccgtacaa cacgctgaag taccccaacg gggaaggagg actgggcgag 240
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 36 gaggacggag tctactggaa gtactgtgaa attcctgcct gccagatgcc tggaaacctt 360
 37 ggctgctaca aggatcatgg aaaccacact cctctcacgg gcaccagtaa aacctctaac 420
 38 aagctcacca tacaacctg tatcagcttc tgcggagtc agagattcaa gtttgctggg 480
 39 atggagtcag gctatgcctg cttctgtggg aacaatcctg actactggaa gcacggggag 540
 40 gcggccagca ccgagtgcaa tagtgtctgc ttccggggacc acacgcagcc ctgcggtggg 600
 41 gacggcagga ttatcctctt tgacactctc gtgggcgcct gcggtgggaa ctactcagcc 660
 42 atggcagccg tgggtgtact ccctgacttc cctgacacct acgccactgg cagagtctgc 720
 43 tactggacca tccgggttcc aggagcctct cgcattccatt tcaacttcac cctgtttgat 780
 44 atcagggact ctgcagacat ggtggagctg ctggaaggct acaccaccg cgtcctggtc 840
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 46 ttgtatttct tctctgatcg catcaatcag gccagggat ttgctgtgtt gtaccaagcc 960
 47 accaaggagg aaccgccaca ggagagacct gctgtcaacc agaccctggc agaggtgatc 1020
 48 accgagcaag ccaacctcag tgtcagcgct gccactcct ccaaagtcct ctatgtcatc 1080
 49 acccccagcc ccagccaccc tccgcagact gccccaggta gccattcctg ggcaccgtca 1140
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 51 atcctcacag tcacagcagt tgtcgcaaag attcttctgc atgtcacatt taaatctcat 1260
 52 cgagtcacct cctcaggaga ccttagggac ttgcgtcagc ctggggcttc tggagatata 1320
 53 tggaccattt tctatgaacc ttccactaca atctccatct ttaagaagaa gctcaagggt 1380
 54 cagagtcaac aagatgaccg caatcccctc gtgagtgact ga 1422

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57 <210> SEQ ID NO: 2

58 <211> LENGTH: 1422

59 <212> TYPE: DNA

60 <213> ORGANISM: Homo sapiens

62 <400> SEQUENCE: 2

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65 aggggaacac agaactggac agcactacaa ggcgggaagc catgtctgtt ttggaacgag 180
66 actttccagc atccatacaa cactctgaaa taccccaacg gggagggggg cctgggtgag 240
67 cacaactatt gcagaaatcc agatggagac gtgagcccct ggtgctatgt ggcagagcac 300
68 gaggatgggtg tctactggaa gtactgtgag atacctgctt gccagatgcc tggaaacctt 360
69 ggctgctaca aggatcatgg aaaccacact cctctaactg gcaccagtaa aacgtccaac 420
70 aaactcacca tacaacttg catcagtttt tgtcggagtc agaggttcaa gtttgctggg 480
71 atggagtcag gctatgcttg cttctgtgga aacaatcctg attactggaa gtacggggag 540
72 gcagccagta ccgaatgcaa cagcgtctgc ttcggggatc acaccaacc ctgtggtggc 600
73 gatggcagga tcatcctctt tgacactctc gtgggcgcct gcggtgggaa ctactcagcc 660
74 atgtcttctg tgggtctatt ccctgacttc cccgacacct atgccacggg gagggctctg 720
75 tactggacca tccgggttcc gggggcctcc cacatccact tcagcttccc cctatttgac 780
76 atcagggact cggcggacat ggtggagctt ctggatggct acaccaccg tgtcctagcc 840
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78 ttgtatttct tctctgatcg catcaatcag gcccagggat ttgctgtttt ataccaagcc 960
79 gtcaaggaag aactgccaca ggagaggccc gctgtcaacc agacggtggc cgaggtgatc 1020
80 acggagcagg ccaacctcag tgtcagcgct gcccggtcct ccaaagtcct ctatgtcatc 1080
81 accaccagcc ccagccaccc acctcagact gtcccaggta gcaattcctg ggcgccaccc 1140
82 atgggggctg gaagccacag agttgaagga tggacagtct atggtctggc aactctcttc 1200
83 atcctcacag tcacagccat tgtagcaaa atacttctgc acgtcacatt caaatcccat 1260
84 cgtgttccctg cttcagggga ccttagggat tgtcatcaac cagggacttc gggggaaatc 1320
85 tggagcattt tttaagaagc ttccacttca atttccatct ttaagaagaa actcaagggt 1380
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90 <211> LENGTH: 1386

91 <212> TYPE: DNA

92 <213> ORGANISM: Mus musculus

94 <400> SEQUENCE: 3

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96 ggggcctcag cagggagcct gcacagtcca ggcttgtccg aatgcttcca ggtgaacggc 120
97 gctgactacc gagggcacca gaactacacc gggccacgag gagctggacg cccttgtctt 180
98 ttctgggacc agacacagca gcacagctac agcagcgcca gcgacctca gggccgctgg 240
99 ggggttgggtg cgcataactt ctgtaggaac ccagacggtg atgtgcagcc ctggtgctac 300
100 gtggcagaga cagaagaggg catctactgg cgctactgtg atatccccac atgtcacatg 360
101 cctgggtacc tgggtgctt cgtggactct ggggcacccc ctgctctcag tggccccagt 420
102 ggcacctcca caaagctcac tgtccaagtg tgccttcgat tctgccgat gaagggtac 480
103 cagctggctg gtgtggaggc tggttatgcc tgcctctgtg gctctgaaag tgacctggcc 540
104 cgcggacgtc cagcccctgc caccgactgt gaccagatct gttttggcca ccaggccag 600
105 ctctgtggag gcgatggacg actaggtatc tatgaagtgt ctgtgggctc ctgccaggga 660
106 aactgggtcg ctcctcaagg agtcatctac tcccggatt ttccggatga gtatggacca 720
107 gaccggaact gcagctgggt attgggcca ctgggcgctg tgctagaact caccttccgc 780
108 ctcttcagat tggctgattc tcgagaccgg ctggagctac gcgacgtctc gtccggcaac 840
109 ctactccgtg ccttcgacgg cgcccatccg ccgcctccgg gaccgctgag cctgcgcact 900

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110 gctgcgctgc tgctcacctt ccgcagcgac gcaagaggcc atgctcaagg ctctcgctc 960
111 acctaccgcg ggctgcagga tacagtggag ggcagagcat ctccagagga ttcaactgag 1020
112 agtctcgagc gggaccccg taggtgccc agtcttctcc accgtgacgg ccttctctgt gctgctgctg 1080
113 caggcttcga taggtgccc agtcttctcc accgtgacgg ccttctctgt gctgctgctg 1140
114 ttgctcctgt ccctactgcg tttgctgctg cgacggagct gtctgctggc tccaggaaaa 1200
115 ggggtctctg ccatgggacc ttcccggggc cccggggaga gctgggctgt gtgggtaccgc 1260
116 cgcccccgag ggggtggccct gccctgtccc ccaggggact ctgaggctga ggggtcctgt 1320
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121 <210> SEQ ID NO: 4

122 <211> LENGTH: 1428

123 <212> TYPE: DNA

124 <213> ORGANISM: Homo sapiens

126 <400> SEQUENCE: 4

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129 ggggctgact accgcggcca ccagaaccgc actggccgc gcggggcggg ccgcccgtgc 180
130 ctcttctggg accagacgca gcaacacagc tacagcagcg ccagcgaccc ccacggccgc 240
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134 agcggcacct ccacgaagct cacgggtccag gtgtgcctac gcttctgccg catgaagggg 480
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137 cagctgtgtg gcggcgatgg gcggtgggc gtctatgaag tgtcggtggg ctctgccag 660
138 gggaaactgga cagcgctca gggcgctcct tactccccgg acttccccga cgagtacggg 720
139 ccggaccgga actgcagctg ggcctgggc ccgccaggcg ccgcgctgga gctcaccttc 780
140 cgcctcttcg agctggccga ccgcgcgac cggtggagc tgcgcgacgc ggcttcgggc 840
141 agcctgctcc gcgcctcga tggcgccgc ccaccgcgt ccgggcccgt gcgcctgggc 900
142 actgcgcgcg ctgtgctcac cttccgaagc gacgcgcgcg gccacgcgca aggttcgcg 960
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145 ccgcggccg cgattggggc ccgggtcttc tcgacgtgga cggtgtctc ggtgctgctg 1140
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147 ctgagggcgg accggtggag ctgtctgctg gctccgggaa aaggggcccc ggcgctggg 1260
148 gcttccaggg gccccaggag aagctgggct gtgtggtacc aacagccccg aggggtggc 1320
149 ttgccctgct cccccgggga cccccaggct gagggttctg ccgcgggcta ccggcctctg 1380
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154 <211> LENGTH: 473

155 <212> TYPE: PRT

156 <213> ORGANISM: Mus musculus

158 <400> SEQUENCE: 5

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160 1 5 10 15
162 Thr Leu Ala Ala Arg Pro Ala Pro Gly Pro Arg Ser Gly Pro Glu Cys
163 20 25 30
165 Phe Thr Ala Asn Gly Ala Asp Tyr Arg Gly Thr Gln Ser Trp Thr Ala
166 35 40 45

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168 Leu Gln Gly Gly Lys Pro Cys Leu Phe Trp Asn Glu Thr Phe Gln His
169      50                      55                      60
171 Pro Tyr Asn Thr Leu Lys Tyr Pro Asn Gly Glu Gly Gly Leu Gly Glu
172 65                      70                      75                      80
174 His Asn Tyr Cys Arg Asn Pro Asp Gly Asp Val Ser Pro Trp Cys Tyr
175                      85                      90                      95
177 Val Ala Glu His Glu Asp Gly Val Tyr Trp Lys Tyr Cys Glu Ile Pro
178                      100                      105                      110
180 Ala Cys Gln Met Pro Gly Asn Leu Gly Cys Tyr Lys Asp His Gly Asn
181                      115                      120                      125
183 Pro Pro Pro Leu Thr Gly Thr Ser Lys Thr Ser Asn Lys Leu Thr Ile
184 130                      135                      140
186 Gln Thr Cys Ile Ser Phe Cys Arg Ser Gln Arg Phe Lys Phe Ala Gly
187 145                      150                      155                      160
189 Met Glu Ser Gly Tyr Ala Cys Phe Cys Gly Asn Asn Pro Asp Tyr Trp
190                      165                      170                      175
192 Lys His Gly Glu Ala Ala Ser Thr Glu Cys Asn Ser Val Cys Phe Gly
193                      180                      185                      190
195 Asp His Thr Gln Pro Cys Gly Gly Asp Gly Arg Ile Ile Leu Phe Asp
196                      195                      200                      205
198 Thr Leu Val Gly Ala Cys Gly Gly Asn Tyr Ser Ala Met Ala Ala Val
199 210                      215                      220
201 Val Tyr Ser Pro Asp Phe Pro Asp Thr Tyr Ala Thr Gly Arg Val Cys
202 225                      230                      235                      240
204 Tyr Trp Thr Ile Arg Val Pro Gly Ala Ser Arg Ile His Phe Asn Phe
205                      245                      250                      255
207 Thr Leu Phe Asp Ile Arg Asp Ser Ala Asp Met Val Glu Leu Leu Asp
208                      260                      265                      270
210 Gly Tyr Thr His Arg Val Leu Val Arg Leu Ser Gly Arg Ser Arg Pro
211                      275                      280                      285
213 Pro Leu Ser Phe Asn Val Ser Leu Asp Phe Val Ile Leu Tyr Phe Phe
214 290                      295                      300
216 Ser Asp Arg Ile Asn Gln Ala Gln Gly Phe Ala Val Leu Tyr Gln Ala
217 305                      310                      315                      320
219 Thr Lys Glu Glu Pro Pro Gln Glu Arg Pro Ala Val Asn Gln Thr Leu
220                      325                      330                      335
222 Ala Glu Val Ile Thr Glu Gln Ala Asn Leu Ser Val Ser Ala Ala His
223                      340                      345                      350
225 Ser Ser Lys Val Leu Tyr Val Ile Thr Pro Ser Pro Ser His Pro Pro
226                      355                      360                      365
228 Gln Thr Ala Pro Gly Ser His Ser Trp Ala Pro Ser Val Gly Ala Asn
229 370                      375                      380
231 Ser His Arg Val Glu Gly Trp Thr Val Tyr Gly Leu Ala Thr Leu Leu
232 385                      390                      395                      400
234 Ile Leu Thr Val Thr Ala Val Val Ala Lys Ile Leu Leu His Val Thr
235                      405                      410                      415
237 Phe Lys Ser His Arg Val Pro Ala Ser Gly Asp Leu Arg Asp Cys Arg
238                      420                      425                      430
240 Gln Pro Gly Ala Ser Gly Asp Ile Trp Thr Ile Phe Tyr Glu Pro Ser

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241          435          440          445
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244          450          455          460
246 Asp Asp Arg Asn Pro Leu Val Ser Asp
247 465          470
250 <210> SEQ ID NO: 6
251 <211> LENGTH: 473
252 <212> TYPE: PRT
253 <213> ORGANISM: Homo sapiens
255 <400> SEQUENCE: 6
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259 Thr Leu Ala Ala Arg Pro Ala Pro Ser Pro Gly Leu Gly Pro Glu Cys
260          20          25          30
262 Phe Thr Ala Asn Gly Ala Asp Tyr Arg Gly Thr Gln Asn Trp Thr Ala
263          35          40          45
265 Leu Gln Gly Gly Lys Pro Cys Leu Phe Trp Asn Glu Thr Phe Gln His
266          50          55          60
268 Pro Tyr Asn Thr Leu Lys Tyr Pro Asn Gly Glu Gly Gly Leu Gly Glu
269 65          70          75          80
271 His Asn Tyr Cys Arg Asn Pro Asp Gly Asp Val Ser Pro Trp Cys Tyr
272          85          90          95
274 Val Ala Glu His Glu Asp Gly Val Tyr Trp Lys Tyr Cys Glu Ile Pro
275          100          105          110
277 Ala Cys Gln Met Pro Gly Asn Leu Gly Cys Tyr Lys Asp His Gly Asn
278          115          120          125
280 Pro Pro Pro Leu Thr Gly Thr Ser Lys Thr Ser Asn Lys Leu Thr Ile
281          130          135          140
283 Gln Thr Cys Ile Ser Phe Cys Arg Ser Gln Arg Phe Lys Phe Ala Gly
284 145          150          155          160
286 Met Glu Ser Gly Tyr Ala Cys Phe Cys Gly Asn Asn Pro Asp Tyr Trp
287          165          170          175
289 Lys Tyr Gly Glu Ala Ala Ser Thr Glu Cys Asn Ser Val Cys Phe Gly
290          180          185          190
292 Asp His Thr Gln Pro Cys Gly Gly Asp Gly Arg Ile Ile Leu Phe Asp
293          195          200          205
295 Thr Leu Val Gly Ala Cys Gly Gly Asn Tyr Ser Ala Met Ser Ser Val
296          210          215          220
298 Val Tyr Ser Pro Asp Phe Pro Asp Thr Tyr Ala Thr Gly Arg Val Cys
299 225          230          235          240
301 Tyr Trp Thr Ile Arg Val Pro Gly Ala Ser His Ile His Phe Ser Phe
302          245          250          255
304 Pro Leu Phe Asp Ile Arg Asp Ser Ala Asp Met Val Glu Leu Leu Asp
305          260          265          270
307 Gly Tyr Thr His Arg Val Leu Ala Arg Phe His Gly Arg Ser Arg Pro
308          275          280          285
310 Pro Leu Ser Phe Asn Val Ser Leu Asp Phe Val Ile Leu Tyr Phe Phe
311          290          295          300
313 Ser Asp Arg Ile Asn Gln Ala Gln Gly Phe Ala Val Leu Tyr Gln Ala

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